



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: Hadlaczky, Gyula  
Szalay, Aladar
- (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Heller Ehrman White & McAuliffe
  - (B) STREET: 4350 La Jolla Village Drive, 6th Floor
  - (C) CITY: San Diego
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US/09/836,911
  - (B) FILING DATE: 17-APR-2001
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/835,682
  - (B) FILING DATE: 10-APR-1997
  - (A) APPLICATION NUMBER: 08/695,191
  - (B) FILING DATE: 07-AUG-1996
  - (A) APPLICATION NUMBER: 08/682,080
  - (B) FILING DATE: 15-JUL-1996
  - (A) APPLICATION NUMBER: 08/629,822
  - (B) FILING DATE: 10-APR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Seidman, Stephanie L
  - (B) REGISTRATION NUMBER: 33,779
  - (C) REFERENCE/DOCKET NUMBER: 24601-402I
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 858-450-8403
  - (B) TELEFAX: 858-587-5360
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1293 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCCATGA	TTTTAAGTTT	60
TCTCGCCATA	TTCCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTTNCACGTT	TTNCAGTGAT	120
TTCGTCAATT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTTC	AGTTTTCTCTC	240
GCCATATTTT	ACGTCCTAAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTCCAG	GTCCTATAAT	GTGCATTTCT	CATTTNMCAC	GTTTTTCAGT	GATTTCGTCA	360
TTTTTTCAAG	TCGGCAAGTG	GATGTTTCTC	ATTTNCCATG	ATTTCAGTT	TTCTTGNAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTTAAT	TTTCCACCTT	TTCATTTTTT	CACGCCATAT	480
TTCATGTCCT	AAAGTGTATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTTCT	CGCCATATTC	540
CAGGTCCCTAC	AGTGTGCATT	CCTCATTTTT	CACCTTTTTT	ACTGATTTCG	TCATTTTTTCA	600
AGTCGTCAAC	TGGATCTTTT	TAATTTTCCA	TGATTTTCAG	TTATCTTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTTCTA	AATTTTCCAA	CTTTTTCAAT	TTTTCTCGAC	ATATTTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTTCACG	TTTTTCAGTGA	TTTCGTCATT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTTT	CTTGCTATAT	TCCATGTCTCT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTTT	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCCTT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTT	ACGTTTTTCA	GTAATTTCTT	CATTTTTTTAA	GCCCTCAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTTCAG	TCCTAAAGTG	1200
TGATTTCTTA	ATTTTCAGTG	ATTTTCAGTT	TTTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTTTCAGTT	TTTCAGTGAA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1044 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAAACT	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTTGAA	GCTTTCTTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
ACACTCTTTT	TTGTAGTATC	TGGAAGTGGA	CATTTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTTG	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTTGTCT	AGCTTTGAGG	ATTTGTTGG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTTCC	AGAACTTCT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660
GGATGTGGAC	ATTGTCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720
AACATAGACAG	AAGCATTTCT	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAACAGTGTT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTGA	AACACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
CATTCCCAGA	ATCTTGTTTG	TGATGTTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCCTTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGGTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCTG	TAGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGGC	GTATTTTGGT	GTGTTCCACT	GGCAATGAAA		900
AGAGTTCTTG	TTTTTCCTTC	AGCAATTTGT	CATTTTAAAA	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTGTG	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTCTTGN	NTTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTATTTG	CAAATATTTT	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCACTTC	1260
TTTTGTGTAT	ATCTACCTTT	TGTGTCAATT	GTTAAAAATC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAA	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTTT	CGTCTATATC	CATATCATT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACCTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATT	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATT	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAAT	GCATCGCTCA	GTCCCACTCC	TCCCTATTTT	TCTACAATAA	ACTCTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280
TTGAATTTAC	AGAAGTATG	GGCTTAATAA	CTGGCGCTCT	GACTTTTAGT	GTGCAGGAGG	2340
CCGTACACAC	GGGACCAAGA	GTGCCCTGCC	TAGTCCCAT	CTGCCCCGAG	GTGGCGGCTG	2400
CCTCGACACT	GACAGCAATA	GGGTCCGGCA	GTGTCCCCAG	CTGCCAGCAG	GGGGCGTACG	2460
ACGACTACAC	TGTGAGCAAG	AGGGCCCTGC	AG			2492

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA

28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Gemomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

47

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (D) OTHER INFORMATION IL-2 signal sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	TAC	AGG	ATG	CAA	CTC	CTG	TCT	TGC	ATT	GCA	CTA	AGT	CTT	GCA	CTT	48
Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu	
1				5				10						15		

GTC	ACA	AAC	AGT	GCA	CCT	ACT	69
Val	Thr	Asn	Ser	Ala	Pro	Thr	
						20	

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...942
  - (D) OTHER INFORMATION: Renilla Reinformis Luciferase
- (x) PUBLICATION INFORMATION:
  - (H) Document Number: 5,418,155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC Ser 1	TTA Leu	AAG Lys	ATG Met	ACT Thr 5	TCG Ser	AAA Lys	GTT Val	TAT Tyr	GAT Asp 10	CCA Pro	GAA Glu	CAA Gln	AGG Arg	AAA Lys 15	CGG Arg	48
ATG Met	ATA Ile	ACT Thr 20	GGT Gly	CCG Pro	CAG Gln	TGG Trp	TGG Trp 25	GCC Ala	AGA Arg	TGT Cys	AAA Lys	CAA Gln 30	ATG Met	AAT Asn	GTT Val	96
CTT Leu	GAT Asp	TCA Ser 35	TTT Phe	ATT Ile	AAT Asn	TAT Tyr 40	TAT Tyr	GAT Asp	TCA Ser	GAA Glu	AAA Lys 45	CAT His	GCA Ala	GAA Glu	AAT Asn	144
GCT Ala 50	GTT Val	ATT Ile	TTT Phe	TTA Leu	CAT His	GGT Gly 55	AAC Asn	GCG Ala	GCC Ala	TCT Ser	TCT Ser 60	TAT Tyr	TTA Leu	TGG Trp	CGA Arg	192
CAT His 65	GTT Val	GTG Val	CCA Pro	CAT His	ATT Ile 70	GAG Glu	CCA Pro	GTA Val	GCG Ala 75	CGG Arg	TGT Cys	ATT Ile	ATA Ile	CCA Pro	GAT Asp 80	240
CTT Leu	ATT Ile	GGT Gly	ATG Met 85	GGC Gly	AAA Lys	TCA Ser	GGC Gly	AAA Lys 90	TCT Ser	GGT Gly	AAT Asn	GGT Gly	TCT Ser	TAT Tyr 95	AGG Arg	288
TTA Leu	CTT Leu	GAT Asp	CAT His 100	TAC Tyr	AAA Lys	TAT Tyr	CTT Leu	ACT Thr 105	GCA Ala	TGG Trp	TTG Leu	AAC Asn	TTC Phe 110	TTA Leu	ATT Ile	336
TAC Tyr	CAA Gln 115	AGA Arg	AGA Arg	TCA Ser	TTT Phe	TTT Phe 120	GTC Val	GGC Gly	CAT His	GAT Asp	TGG Trp	GGT Gly 125	GCT Ala	TGT Cys	TTG Leu	384
GCA Ala 130	TTT Phe	CAT His	TAT Tyr	AGC Ser	TAT Tyr	GAG Glu 135	CAT His	CAA Gln	GAT Asp	AAG Lys	ATC Ile 140	AAA Lys	GCA Ala	ATA Ile	GTT Val	432
CAC His 145	GCT Ala	GAA Glu	AGT Ser	GTA Val 150	GTA Val	GAT Asp	GTG Val	ATT Ile	GAA Glu 155	TCA Ser	TGG Trp	GAT Asp	GAA Glu	TGG Trp	CCT Pro 160	480
GAT Asp	ATT Ile	GAA Glu	GAA Glu	GAT Asp 165	ATT Ile	GCG Ala	TTG Leu	ATC Ile	AAA Lys 170	TCT Ser	GAA Glu	GAA Glu	GGA Gly 175	GAA Glu	AAA Lys	528
ATG Met	GTT Val	TTG Leu 180	GAG Glu	AAT Asn	AAC Asn	TTC Phe	TTC Phe 185	GTG Val	GAA Glu	ACC Thr	ATG Met	TTG Leu	CCA Pro 190	TCA Ser	AAA Lys	576
ATC Ile	ATG Met	AGA Arg 195	AAG Lys	TTA Leu	GAA Glu	CCA Pro	GAA Glu 200	GAA Glu	TTT Phe	GCA Ala	GCA Ala	TAT Tyr 205	CTT Leu	GAA Glu	CCA Pro	624
TTC Phe 210	AAA Lys	GAG Glu	AAA Lys	GGT Gly	GAA Glu	GTT Val 215	CGT Arg	CGT Arg	CCA Pro	ACA Thr	TTA Leu 220	TCA Ser	TGG Trp	CCT Pro	CGT Arg	672
GAA Glu 225	ATC Ile	CCG Pro	TTA Leu	GTA Val	AAA Lys 230	GGT Gly	GGT Gly	AAA Lys	CCT Pro	GAC Asp 235	GTT Val	GTA Val	CAA Gln	ATT Ile	GTT Val 240	720
AGG Arg	AAT Asn	TAT Tyr	AAT Asn 245	GCT Ala	TAT Tyr	CTA Leu	CGT Arg	GCA Ala 250	AGT Ser	GAT Asp	GAT Asp	TTA Leu	CCA Pro	AAA Lys 255	ATG Met	768
TTT Phe	ATT Ile	GAA Glu	TCG Ser 260	GAT Asp	CCA Pro	GGA Gly	TTC Phe 265	TTT Phe	TCC Ser	AAT Asn	GCT Ala	ATT Ile	GTT Val 270	GAA Glu	GGC Gly	816

GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT	864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His	
275 280 285	
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG	912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser	
290 295 300	
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA	945
Phe Val Glu Arg Val Leu Lys Asn Glu Gln	
305 310	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG 30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTCAC 30

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1434 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC AGAGCAGCGT TGGGGGATAA 60

TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	GA CTGACACC	ATTAACACTT	TGTCAGCCTC	AGTGA CTACA	GTCATAGATG	240
AACAGGCCTC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTCCA	GATACAAC TA	GATGTATTAT	GACAAATAAC	TCAGCAGGGA	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATT C	AGTATGT TAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAAG	TCTTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGAATTT	GAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGGA	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAATTG	GATCTCCTCA	GCATTTTCTT	TCTTTAAAAA	ATGGGTGGGA	TTAATATTAT	600
TTGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGGTCTGT	AAGCTTAAGG	660
CCCAAACTAG	GAGAGACAA G	GTGGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGAG	TGTGCTTCAG	CAGCCCGAGA	840
GAGTTGCAAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTTCAT	GAAGGTTTCA	TGTCCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGT	AGGTCAGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCCTG	1020
TACATGGCTC	CTTTACCTAC	ACACTGGGGA	TTTGACCTCT	ATCTCCACTC	TCATTAATAT	1080
GGGTGGCCTA	TTTGCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GTTGGGAGCC	GCGCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTTCTAAGTG	GTAACAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GTGGTCTTTC	ACTCCATGTG	TCTTGCCTTC	CCCGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCCTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTCT	CTCTCTCTCT	TGCTTCTCTC	TCTTGCTTTT	TCGCTCTCTT	1380
GCTTCCCGTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	ACA ACTAGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240
TTCCGGGATT	GCGTGT TATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTTGT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTTGAA	CAGATCCTTC	360
GGGAATTGAG	ACTTCAGGTC	AACTCCACGC	GCTTGGACCT	GTCCCTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTTCTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTTG	480
GAGATACACT	TTGCTGTGGA	TTAGTGTTGC	TTCTTTGATT	GGTCTGTAAG	CCTAAGGCCC	540
AAACTAGGAG	AGACAAGGTG	GTTATTGCCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	600
CCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TCGCTGGCCA	CTCAGCTCTT	ATATCCCATG	660
AGGCTAGTCT	CATTGCACGG	GATAGAGTGA	GTGTGCTTCA	GCAGCCCGAG	AGAGTTGCAC	720
GGCTAAGCAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCATCTTTCA	AGAAGGTTGA	GTGTCCAAGT	GTCTTCTCTC	CAGGCAAAAC	GACACGGGAG	840
CAGGTCAGGG	TTGCTCTGGG	TAAAAGCCTG	TGAGCCTAAG	AGCTAATCCT	GTACATGGCT	900
CCTTTACCTA	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	960
ATTTGCTCTT	ATTAAAAGGA	AAGGGGGAGA	TGTTGGGAGC	CGCGCCCACA	TTCGCCGTTA	1020
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGCGC	ATGCGCCGAG	1080
GGTGGTTCTT	CACTCCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCAATCA	GGGAGTGACA	CGTCCTAGGC	GAAGGAAAAT	TCTCCTTAAT	AGGGACGGGG	1200
TTTCGTTTTT	TCTCTCTCTT	GCTTCGCTCT	CTCTTGCTTC	TTGCTCTCTT	TTCTTGAAGA	1260
TGTAAGAATA	AAGCTTTTGC	GCAGAAGATT	CTGGTCTGTG	GTGTTCTTCC	TGGCCGGTCG	1320
TGAGAACGCG	TCTAATAACA	ATTGGTGCCG	AAACCCGGGT	GATAATGATT	ATCATCTACA	1380
TATCACAACG	TGCGTGGAGG					1400

(2) INFORMATION FOR SEQ ID NO:15:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	ACTTTACGGG	TCCTTTCCT	60
ACAACCTGCCA	CGAGGCCCCG	TGCTCTGGTA	ATAGATCTTT	GCTGAAAAGG	CACACACATG	120
ACACATTACT	CAAGGTGGGC	TCATCTGAGC	TGCAGATTCA	GCTTAATATG	AATCTTGCCA	180
ATTGTGTGAA	ATCATAAATC	TTCAAAGTGA	CACTCATTGC	CAGACACAGG	TGCCCCACCTT	240
TGGCATAATA	AACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTTGAGAGCT	TAAATTTAAT	AAAGTGATAT	360
ACCTAATAAA	AATTAAATTA	AGAAGGTGTG	AATATACTAC	AGTAGGTAAA	TTATTTTCATT	420
AATTTATTTT	CTTTCTTAAT	CCTTTATAAT	GTTTTCTGCT	ATTGTCAATT	GCACATCCAT	480
ATGTTCAATT	CTTCACTGTA	ATGAAGAAAT	GTAGTAAATA	TACTTTCCGA	ACAAGTTGTA	540
TCAAATATGT	TACACTTGAT	TCCGTGTGTT	ACTTATCATT	TTATTATTAT	ATTGATTGCA	600
TTCTTTCGTT	ACTTGATATT	ATTACAAGGT	ACATATTTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACCAT	TTTATAACAT	ACTTTATTTA	TTCATTTCTT	ATGTGTGCTG	TGAGGCACAA	720
ATGCCAGAGA	GAACCTGAGC	AGATAAGAGG	ACAAATTGCA	AGAGTCAGTT	ACCTCCTGCT	780
GTCCTTGGA	AACTCAGGAT	CAAATTCAGG	TTGTCAGGCT	TGGCAGCATG	CACTTTTTTAC	840
CAGTGCCCTC	ATCTTGCTAG	CCCTGAACAT	CAAGCTTTGC	AGACAGACAG	GCTACACTAA	900
GTGAACGGT	CATTCACAGC	ATGCATGGTG	ATTTATTGTT	ACTTTCTATT	CCATGCCTTT	960
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTTTCGAGA	TAGAAGTTAC	TGAAAGAAAA	1020
TTACATTGTT	TTCTATAGAT	CCTTGATACT	CTTTCAGCAG	ATATAGAGTT	TTAATCAGGT	1080
CCTAGACCCT	TTCTTCACTC	TTATTAAATA	CTAAGTACAA	ATTAAGTTTA	TCCAAAACAG	1140
TACGGATGTT	GATTTTGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1200
CACTTATTGG	GAATGTTTTT	GTTAATAAAA	GATTCAGGTG	TTACTCTAGG	TCAAGAGAAT	1260
ATTAAACATC	AGTCCCAAAT	TACAAACTTC	AATAAAAGAT	TTGACTCTCC	AGTGGTGGCA	1320
ATATAAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACGT	GCGTGGAGG		1369

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22118 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCTCT	ATCCCTAATC	CAGATTGGTG	GAATAACTTG	GTATAGATGT	TTGTGCATTA	60
AAAACCTCTG	AGGATCTTCA	CTCTAGGTCA	CTGTTACAGC	CTGGAACCTG	AATTGTGGCC	120
CTGAGTGATA	GGTCCTGGGA	CATATGCAGT	TCTGCACAGA	CAGACAGACA	GACAGACAGA	180
CAGACAGACA	GACAGACGTT	ACAAACAAAC	ACGTTGAGCC	GTGTGCCAAC	ACACACACAA	240
ACACCACTCT	GGCCATAATT	ATTGAGGACG	TTGATTTATT	ATTCTGTGTT	TGTGAGTCTG	300
TCTGTCTGTC	TGTCTGTCTG	TCTGTCTGTC	TATCAAACCA	AAAGAAACCA	AACAATTATG	360
CCTGCCTGCC	TGCCTGCCTG	CCTACACAGA	GAAATGATTT	CTTCAATCAA	TCTAAAACGA	420
CCTCCTAAGT	TTGCCTTTTT	TCTCTTTCTT	TCTTTTCTTT	TTTCTTTCTT	TCTTCTTCTT	480
TCCTTCCTTC	CTTCTTCCTT	TCCTTCCTTT	CTTCTTTCTT	TTCTTTCTTT	CTTACTTTCT	540
TTCTTTCTTT	CTTACATTTA	TTCTTTTCAT	ACATAGTTTC	TTAGTGTAAG	CATCCCTGAC	600
TGTCTTGAAG	ACACTTTGTA	GGCCTCAATC	CTGTAAGAGC	CTTCCTCTGC	TTTTTCAAATG	660
CTGGCATGAA	TGTTGTACCT	CACTATGACC	AGCTTAGTCT	TCAAGTCTGA	GTTACTGGAA	720
AGGAGTTCCA	AGAAGACTGG	TTATATTTTT	CATTTATTAT	TGCATTTTAA	TTAAAATTTA	780

ATTTACCAA	AAGAATTTAG	ACTGACCAAT	TCAGAGTCTG	CCGTTTAAAA	GCATAAGGAA	840
AAAGTAGGAG	AAAAACGTGA	GGCTGTCTGT	GGATGGTCTGA	GGCTGCTTTA	GGGAGCCTCG	900
TCACCATTCT	GCACTTGCAA	ACCGGGCCAC	TAGAACCCGG	TGAAGGGAGA	AACCAAAGCG	960
ACCTGGAAC	AATAGGTCAC	ATGAAGGCCA	GCCACCTCCA	TCTTGTTGTG	CGGGAGTTCA	1020
GTTAGCAGAC	AAGATGGCTG	CCATGCACAT	GTTGTCTTTC	AGCTTGGTGA	GGTCAAAGTA	1080
CAACCGAGTC	ACAGAACAAG	GAAGTATACA	CAGTGAGTTC	CAGGTCAGCC	AGAGTTTACA	1140
CAGAGAAACC	ACATCTTGAA	AAAAACAAAA	AAATAAATTA	AATAAATATA	ATTTAAAAAT	1200
TTAAAAATAG	CCGGGAGTGA	TGGCGCATGT	CTTTAATCCC	AGCTCTCTTC	AGGCAGAGAT	1260
GGGAGGATTT	CTGAGTTTGA	GGCCAGCCTG	GTCTGCAAAG	TGAGTTCCAG	GACAGTCAGG	1320
GCTATACAGA	AAAACCCTGT	CTTGAAAAC	AAACTAAAT	AAACTAAACT	AAACTAAAAA	1380
AATATAAAAT	AAAAATTTTA	AAGAATTTTA	AAAAACTACA	GAAATCAAAC	ATAAGCCAC	1440
GAGATGGCAA	GTAAC TGCAA	TCATAGCAGA	AATATTATAC	ACACACACAC	ACACAGACTC	1500
TGTCATAAAA	TCCAATGTGC	CTTCATGATG	ATCAAATTTT	GATAGTCAGT	AATACTAGAA	1560
GAATCATATG	TCTGAAAATA	AAAGCCAGAA	CCTTTTCTGC	TTTTGTTTTC	TTTTGCCCCA	1620
AGATAGGTTT	TCTCTCAGTG	TATCCCTGCT	ATCCCTGCCT	GGAACCTCCT	TTGTAGGTTT	1680
GGTAGCCTCA	AAC TCAGAGA	GGTCCTCTCT	GCTCGCTGCT	CTGCCTGCCT	GCCTGCCTGC	1740
CTGCCTGCCT	GCCTGCCTCA	CTTCTTCTGC	CACCCACACA	ACCGAGTCGA	ACCTAGGATC	1800
TTTATTTCTT	TCTCTTTCTC	TCTTCTTTCT	TTCTTCTTTT	CTTCTTTCTT	TTCTTTCTTT	1860
CTTTCTTTCT	TTCTTATTCA	ATTAGTTTTT	AATGTAAGTG	TGTGTTTGTG	CTCTATCTGC	1920
TGCCTATAGG	CCTGCTTGCC	AGGAGAGGGC	AACAGAACCT	AGGAGAAACC	ACCATGCAGC	1980
TCCTGAGAAT	AAGTGAAAAA	ACAACAAAAA	AAGGAAATTC	TAATCACATA	GAATGTAGAT	2040
ATATGCCGAG	GCTGTTCAGAG	TGCTTTTAA	GGCTTAGTGT	AAGTAATGAA	AATTGTTGTG	2100
TGTCTTTTAT	CCAAACACAG	AAGAGAGGTG	GCTCGGCCCT	CATGTCGTGT	GTCTGCATGT	2160
AGACCAGGCT	GGCCTTGAAC	ACATTAATCT	GTCTGCCTCT	GCTTCCCTAA	TGCTGCGATT	2220
AAAGCCATGT	GCCACCACTG	CCCGGACTGA	TTTCTTCTTT	TTTTTTTTTT	TGGAAAAATAC	2280
CTTCTTTCTT	TTTTCTCTCT	CTCTTTCTTC	CTTCTTCTCT	TTCTTTCTAT	TCTTTTTTTC	2340
TTTCTTTTTT	TTTTTTTTTT	TTTTTTTTTAA	AATTTGCCCTA	AGGTTAAAGG	TGTGCTCCAC	2400
AATTGCCCTCA	GCTCTGCTCT	AATTCTCTTT	AAAAAAAAAAC	AAACAAAAAA	AAAACCAAAA	2460
CAGTATGTAT	GTATGTATAT	TTAGAAGAAA	TACTAATCCA	TTAATAACTC	TTTTTTCCTA	2520
AAATTCATGT	CATTCTTGTT	CCACAAAGTG	AGTTCCAGGA	CTTACCAGAG	AAACCCTGTG	2580
TTCAAATTTT	TGTGTTCAAG	GTCACCCTGG	CTTACAAAGT	GAGTTCCAAG	TCCGATAGGG	2640
CTACACAGAA	AAACCATATC	TCAGAAAAAA	AAAAAGTTCC	AAACACACAC	ACACACACAC	2700
ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAG	CGCGCCGCGG	CGATGAGGGG	2760
AAGTCGTGCC	TAAAATAAAT	ATTTTTCTGG	CCAAAGTGAA	AGCAAATCAC	TATGAAGAGG	2820
TACTCCTAGA	AAAAATAAAT	ACAAACGGGC	TTTTTAATCA	TTCCAGCACT	GT'TTTAATTT	2880
AACTCTGAAT	TTAGTCTTGG	AAAAGGGGGC	GGGTGTGGGT	GAGTGAGGGC	GAGCGAGCAG	2940
ACGGCGGGGC	GGGCGGGTGA	GTGGCCGGCG	GCGGTGGCAG	CGAGCACCAG	AAAACAACAA	3000
ACCCCAAGCG	GTAGAGTGTT	TTAAAAATCG	GACCTAAATG	TGGTGGAAAC	GAGGTGCGCG	3060
CCACCCTCCT	CTTCCACTGC	TTAGATGCTC	CCTTCCCCTT	ACTGTGCTCC	CTTCCCCTAA	3120
CTGTGCCTAA	CTGTGCCTGT	TCCCTCACCC	CGCTGATTCT	CCAGCGACGT	ACTTTGACTT	3180
CAAGAACGAT	TTTGCTGTGT	TTCACCGCTC	CCTGTATATC	TTTCGTTTTT	GGGTGCCCGA	3240
GTCTAGCCCG	TTGCTATGT	TCGGGCGGGA	CGATGGGGAC	CGTTTGTGCC	ACTCGGGAGA	3300
AGTGGTGGGT	GGGTACGCTG	CTCCGTCGTG	CGTGGCTGAG	TGCCGGAACC	TGAGCTCGGG	3360
AGACCCTCCG	GAGAGACAGA	ATGAGTGAGT	GAATGTGGCG	GCGCGTGACG	GATCTGTATT	3420
GGTTTGATATG	GTTGATCGAG	ACCATTGTCT	GGCGACACCT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTCCAGG	CCTCTCAGGT	TGGTGACACA	GGAGAGGGAA	GTGCCTGTGG	TGAGGCGACC	3540
AGGGTGACAG	GAGGCCGGGC	AAGCAGGCGG	GAGCGTCTCG	GAGATGGTGT	CGTGT'TTAAG	3600
CAGGGTCTCT	AACAAGGAGG	TCGTACAGGG	AGATGGCCAA	AGCAGACCGA	GTTGCTGTAC	3660
GCCCTTTTGG	GAAAAATGCT	AGGGTTGGTG	GCAACGTTAC	TAGGTGCGAC	AGAAGGCTTA	3720
AGTCCTACCC	CCCCCCCCCT	TTTTTTTTTT	TTTCTTCCAG	AAGCCCTCTC	TTGTCCCCGT	3780
CACCGGGGGC	ACCGTACATC	TGAGGCCGAG	AGGACGCGAT	GGGCCCCGCT	TCCAAGCCGG	3840
TGTGGCTCGG	CCAGTGGCG	CTTCGGGTCT	TTTTTTTTTT	TTTTTTTTTT	TTTTCTCTCA	3900
GAAGCCTTGT	CTGTGCTGT	CACCGGGGGC	GCTGTACTTC	TGAGGCCGAG	AGGACGCGAT	3960
GGGCCCCGGC	TTCCAAGCCG	GTGTGGCTCG	GCCAGCTGGA	GCTTCGGGTC	TTTTTTTTTT	4020
TTTTTTTTTT	TTTTTTTCTC	CAGAAGCCTT	GTCTGTGCTG	GTCACCGGGG	GCGCTGTACT	4080
TCTGAGGCCG	AGAGGACGCG	ATGGGTCCGG	TTCCAAGCCG	ATGTGGCGGG	GCCAGCTGGA	4140
GCTTCGGGTT	TTTTTTTTTT	CTCCAGAAGC	CCTCTCTTGT	CCCCGTACC	GGGGGCGCTG	4200
TACTTCTGAG	GCCGAGAGGA	CGTGATGGGC	CCGGGTTCCA	GGCGGATGTC	GCCCCTCAG	4260
CTGGAGCTTT	GGATCTTTTT	TTTTTTTTTT	CCTCCAGAAG	CCCTCTCTTG	TCCCCGTCAC	4320
CGGGGGCACC	TTACATCTGA	GGGCGAGAGG	ACGTGATGGG	TCCGGCTTCC	AAGCCGATGT	4380
GGCGGGGCCA	GCTGGAGCTT	CGGGTTTTTT	TTTTTTTCTC	CAGAAGCCCT	CTCTTGTCCT	4440
CGTCACCGGG	GGCGCTGTAC	TTCTGAGGCC	GAGAGGACGT	GATGGGCCCC	GTTTCCAGGC	4500
GGATGTGCGC	CGGTCAGCTG	GAGCTTTGGA	TCATTTTTTT	TTTTCCCTCC	AGAAGCCCTC	4560
TCTTGTCCTC	GTCACCGGGG	GCACCGTACA	TCTGAGGCCG	AGAGGACACG	ATGGGCCTGT	4620
CTTCCAAGCC	GATGTGGCCC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	TTTTTTCCTC	4680
CAGAAGCCTT	GTCTGTGCTG	GTCACCGGGG	GCGCTGTACT	TCTGAGGCCG	AGAGGACGCG	4740
ATGGGCCCCG	CTTCCAAGCC	GGTGTGGCTC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	4800

TTTTTTTTTTT	TTCCTCCAGA	AACCTTGTCT	GTCGCTGTCA	CCCCGGGCGC	TTGTACTTCT	4860
GATGCCGAGA	GGACGCGATG	GGCCCGTCTT	CCAGGCCGAT	GTGGCCCGGT	CAGCTGGAGC	4920
TTTGGATCTT	TTTTTTTTTTT	TTTTCTCTCA	GAAGCCCTCT	CTTGTCCCCG	TCACCGGGGG	4980
CACCTTACAT	CTGAGGCCTA	GAGGACACGA	TGGGCCCCGG	TTCCAGGCCG	ATGTGGCCCC	5040
GTCAGCTGGA	GCTTTGGATC	TTTTTTTTTTT	TTTTCTTCCA	GAAGCCCTCT	TGCCCCCGTC	5100
ACCGGTGGCA	CTGTACATCT	GAGGCGGAGA	GGACATTATG	GGCCCGGCTT	CCAATCCGAT	5160
GTGGCCCGGT	CAGCTGGAGC	TTTGGATCTT	ATTTTTTTTTT	TAATTTTTTTC	TTCCAGAAGC	5220
CCTCTTGTC	CTGTACCCGG	TGGCACGGTA	CATCTGAGGC	CGAGAGGACA	TTATGGGCCC	5280
GGCTTCCAGG	CCGATGTGGC	CCGGTCAGCT	GGAGCTTTGG	ATCTTTTTTTT	TTTTTTTTTCT	5340
TTTTTCCTCC	AGAAGCCCTC	TCTGTCCCTG	TCACCGGGGG	CCCTGTACGT	CTGAGGCCGA	5400
GGGAAAGCTA	TGGGCGCGGT	TTTCTTTTCT	TGACCTGTCT	GTCTTATCAG	TTCTCCGGGT	5460
TGTCAGGGTC	GACCAGTTGT	TCCTTTGAGG	TCCGGTTCTT	TTCTTATATG	GGTCATTTTTT	5520
GGGCCACCTC	CCCAGGTATG	ACTTCCAGGC	GTCGTTGCTC	GCCTGTCACT	TTCTCCCTTG	5580
TCTCTTTTAT	GCTTGTGATC	TTTTCTATCT	GTTTCTATTG	GACCTGGAGA	TAGGTACTGA	5640
CACGCTGTCC	TTTCCCTATT	AACACTAAAG	GACACTATAA	AGAGACCCTT	TCGATTTAAG	5700
GCTGTTTTTG	TTGTCCAGCC	TATTCTTTTTT	ACTGGCTTGG	GTCTGTCCGG	GTGCCTGCAAG	5760
CTGTCCCCGA	GCCACGCTTC	CTGCTTTCCC	GGGCTTGCTG	CTTGCGTGTG	CTTGCTGTGG	5820
GCAGCTTGTG	ACAACCTGGC	GCTGTGACTT	TGCTGCGTGT	CAGACGTTTT	TCCCGATTTT	5880
CCCGAGGTGT	CGTTGTCCAC	CTGTCTCCCG	TTGGAATGGT	GGAGCCAGCT	GTGGTTGAGG	5940
GCCACCTTAT	TTCCGGCTCA	TTTTTTTTTTT	TTTTTTTCTC	TTGGAGTCCC	GAACCTCCCG	6000
TCTTTTCTCT	TCCCGTCTTT	TCTTCCACAT	GCCTCCCGAG	TGCATTTCTT	TTTGTTTTTT	6060
TTCTTTTTTTT	TTTTTTTTTTT	TTGGGGAGGT	GGAGAGTCCC	GAGTACTTCA	CTCCTGTCTG	6120
TGGTGTCCAA	GTGTTTCATG	CACGTGCCTC	CCGAGTGCAC	TTTTTTTTTGT	GGCAGTCGCT	6180
CGTTGTGTTT	TCTTGTCTTG	TGTCTGCCCG	TATCAGTAAC	TGTCTTGCCC	CCGCTGTAAG	6240
ACATTCCATC	CTCGCTTGT	TCTCCCGATT	GCGCGTCGTT	GCTCACTCTT	AGATCGATGT	6300
GGTGCTCCGG	AGTTCTCTTC	GGGCCAGGGC	CAAGCCGCGC	CAGGCGAGGG	ACGGACATTC	6360
ATGGCGAATG	GCGGCCGCTC	TTCTCGTTCT	GCCAGCGGGC	CCTCGTCTCT	CCACCCCATC	6420
CGTCTGCCGG	TGGTGTGTGG	AAGGCAGGGG	TGCGGCTCTC	CGGCCCGACG	CTGCCCGCGC	6480
CGCACTTTTC	TCAGTGGTTC	GCGTGGTCTT	TGTGGATGTG	TGAGGCGCCC	GGTTGTGCCC	6540
TCACGTGTTT	CACTTTGGTC	GTGTCTCGCT	TGACCATGTT	CCCAGAGTCG	GTGGATGTGG	6600
CCGGTGGCGT	TGCATACCCT	TCCCGTCTGG	TGTGTGCACG	CGCTGTTTCT	TGTAAGCGTC	6660
GAGGTGCTCC	TGGAGCGTTC	CAGGTTTGTC	TCCTAGGTGC	CTGCTTCTGA	GCTGGTGGTG	6720
GCGCTCCCCA	TTCCCTGGTG	TGCCTCCGGT	GCTCGGCTCT	GCTGTGTGCC	TTCCCGTTTG	6780
TGTCTGAGAA	GCCCGTGAGA	GGGGGGTCTG	GGAGAGAAGG	AGGGGCAAGA	CCCCCTTCT	6840
TCGTCCGGTG	AGGCGCCAC	CCCGCGACTA	GTACGCCTGT	GCGTAGGGCT	GGTGCTGAGC	6900
GGTCGCGGCT	GGGGTTGGAA	AGTTTCTCGA	GAGACTCATT	GCTTTCCCGT	GGGGAGCTTT	6960
GAGAGGCCTG	GCTTTCGGGG	GGGACCGGTT	GCAGGGTCTC	CCCTGTCCGC	GGATGCTCAG	7020
AATGCCCTTG	GAAGAGAACC	TTCTGTGTGC	CGCAGACCCC	CCCGCGCGGT	CGCCCGCGTG	7080
TTGGTCTTCT	GGTTTCCCTG	TGTGCTCGTC	GCTGCATCC	TCTCTCGGTG	CGCGGGGCTC	7140
GTCGGGGTTT	TGGGTCCGTC	CCGCCCTCAG	TGAGAAAGTT	TCCTTCTCTA	GCTATCTTCC	7200
GGAAAGGGTG	CGGGCTTCTT	ACGGTCTCGA	GGGGTCTCTC	CCGAATGGTC	CCCTGGAGGG	7260
CTCGCCCCCT	GACCGCCTCC	CGCGCGCGCA	GCGTTTGCTC	TCTCGTCTAC	CGCGGCCCGC	7320
GGCCTCCCCG	CTCCGAGTTC	GGGGAGGGAT	CACGCGGGG	AGAGCCTGTC	TGTCGCTCTG	7380
CCGTGCTGTC	GGAGCATGTG	GCTCGGCTTG	TGTGGTTGGT	GGCTGGGGAG	AGGGCTCCGT	7440
GCACACCCCC	GCGTGCGCGT	ACTTTCCTCC	CCTCCTGAGG	GCCGCCGTGC	GGACGGGGTG	7500
TGGGTAGGCG	ACGGTGGGCT	CCCGGGTCCC	CACCCGTCTT	CCCGTGCCCT	ACCCGTGCCT	7560
TCCGTGCGGT	GCGTCCCTCT	CGCTCGCGTC	CACGACTTTG	GCCGCTCCCC	CGACGGCGGC	7620
CTGCGCCGCG	CGTGGTGCGT	GCTGTGTGCT	TCTCGGGCTG	TGTGGTTGTG	TCGCTGCGCC	7680
CCCCCTTCTC	CGCGGCAGCG	TTCCACGGC	TGGCGAAATC	GCGGGAGTCC	TCCTTCCCTT	7740
CCTCGGGGTC	GAGAGGGTCC	GTGTCTGGCG	TTGATTGATC	TCGCTCTCGG	GGACGGGACC	7800
GTTCTGTGGG	AGAACGGCTG	TTGGCCGCGT	CCGGCGCGAC	GTCGGACGTG	GGGACCCACT	7860
GCCGCTCGGG	GGTCTTCGTC	GGTAGGCATC	GGTGTGTGCG	CATCGGTCTC	TCTCTCGTGT	7920
CGGTGTGCGC	TCCTCGGGCT	CCCGGGGGGC	CGTGTGTTT	CGGGTCGGCT	CGGCGCTGCA	7980
GGTGTGGTGG	GACTGCTCAG	GGGAGTGGTG	CAGTGTGATT	CCCGCCGGTT	TTGCCTCGCG	8040
TGCCCTGACC	GGTCCGACGC	CCGAGCGGTC	TCTCGGTCCC	TTGTGAGGAC	CCCCTTCCGG	8100
GAGGGGCCCG	TTTCGGCCGC	CCTTGCCGTC	GTCGCCGGCC	CTCGTTCTGC	TGTGTCTGTT	8160
CCCCCTCCCC	GCTCGCCGCA	GCCGGTCTTT	TTTCTCTCT	CCCCCTCTCT	CCTCTGACTG	8220
ACCCCTGGCC	CTGCTGTGCG	ACCCCCGCA	TGGGGCCGGC	CGGGCACGTA	CCGCTCCGGG	8280
CGGTACCCGG	GGTCTTGGGG	GGGGGCCGAG	GGGTAAGAAA	GTCGGCTCGG	CGGGCGGGAG	8340
GAGCTGTGGT	TTGGAGGGCG	TCCCGGCCCC	GCGGCCGTGG	CGGTGTCTTG	CGCGGTCTTG	8400
GAGAGGGCTG	CGTGCGAGGG	GAAAAGGTTG	CCCCGCGAGG	GCAAAGGGAA	AGAGGCTAGC	8460
AGTGGTCATT	GTCCCGACGG	TGTGGTGGTC	TCTTGGCGGA	GGTGCGTCTG	GGGGGCTCGT	8520
CCGGCCCTGT	CGTCCGTCGG	GAAGGCGCGT	GTTGGGGCCT	GCCGGAGTGC	CGAGGTGGGT	8580
ACCTTGCGCG	TGGGATTAAC	CCCGCGCGCG	TGTCCCGGTG	TGGCGGTGGG	GGCTCCGGTC	8640
GATGCTTACC	TCCCTCTCCC	CGAGGTCTCA	GGCCTTCTCC	GCGCGGGCTC	TCGGCCCTCC	8700
CCTCGTTCC	CCCTCTCGCG	GGGTTCAAGT	CGCTCGTCTG	CCTCCCTCC	TCCGTCTTCT	8760
CATCTCTCGC	GCAATGGCGC	CGCCCGAGTT	CACGGTGGGT	TCGTCTCCG	CCTCCGCTTC	8820

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TGTTCTCACT	CTGCCACCAA	CGCGCTTTGT	ACATTGAATG	TGAGCTTTGT	TTTGCTTAAC	21420
AGACATATAT	TTTTTCTTTT	GGTTTTGCTT	GACATGGTTT	CCCTTTCTAT	CCGTGCAGGG	21480
TTCCCAGACG	GCCTTTTGAG	AATAAAATGG	GAGGCCAGAA	CCAAAGTCTT	TTGAATAAAG	21540
CACCACAAC	CTAACCTGTT	TGGCTGTTTT	CCTTCCCAAG	GCACAGATCT	TTCCCAGCAT	21600
GGAAAAGCAT	GTAGCAGTTG	TAGGACACAC	TAGACGAGAG	CACCAGATCT	CATTGTGGGT	21660
GGTTGTGAAC	CACCCACCAT	GTGGTTGCC	GGGATTTGAA	CTCAGGATCT	TCAGAAGACG	21720
AGTCAGGGG	CTAAACCGAT	GAGCCATCTC	TCCAGCCCTC	CTACATTCTT	TCTTAAGGCA	21780
TGAATGATCC	CAGCATGGGA	AGACAGTCTG	CCCTCTTTGT	GGTATATCAC	CATATACTCA	21840
ATAAAATAAT	GAAATGAATG	AAGTCTCCAC	GTATTTATTT	CTTCGAGCTA	TCTAAATTCT	21900
CTCACAGCAC	CTCCCCCTCC	CCCACACTGC	CTTTCTCCCT	ATGTTTGGGT	GGGGCTGGGG	21960
GAGGGGTGGG	GTGGGGGCAG	GGATCTGCAT	GTCTTCTTGC	AGGTCTGTGA	ACTATTTGCG	22020
ATGGCCTGGT	TCTCTGAAC	GTTGAGCCTT	GTCTATCCAG	AGGCTGACTG	GCTAGTTTTT	22080
TACCTGAAGT	CCCTGAGTGA	TGATTTCCTT	GTGAATTC			22118

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42999 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCCTCTGG	CGACCTGTCTG	TCGGAGAGGT	TGGGCCTCCG	GATGCGCGCG	60
GGGCTCTGGC	CTCACGGTGA	CCGGCTAGCC	GGCCGCGCTC	CTGCCTTGAG	CCGCCTGCCG	120
CGGCCCGCGG	GCCTGCTGTT	CTCTCGCGCG	TCCGAGCGTC	CCGACTCCCG	GTGCCGGCCC	180
GGGTCCGGGT	CTCTGACCCA	CCCCGGGGCG	GCGGGGAAGG	CGGCGAGGGC	CACCGTGCCC	240
CGTGCGCTCT	CCGCTGCGGG	CGCCCCGGGG	GCCGCACAAC	CCCACCCGCT	GGCTCCGTGC	300
CGTGCGTGTC	AGGCGTTCTC	GTCTCCGCGG	GGTTGTCCCG	CGCCCTTTC	CCGGAGTGCG	360
GGGTGGCCGG	AGCCGATCGG	CTCGCTGGCC	GGCCGGCCTC	CGCTCCCGGG	GGGCTCTTCG	420
ATCGATGTGG	TGACGTCTGT	CTCTCCCGGG	CCGGGTCCGA	GCCGCGACGG	GCGAGGGGCG	480
GACGTTCTGT	GCGAACGGGA	CCGTCTTTCT	CGTCCGCC	GCGCGGTCCC	CTCGTCTGCT	540
CCTCTCCCC	CCCGCCGGC	GGCGTGTGGG	AAGGCGTGGG	GTGCGGACCC	CGGCCCGACC	600
TCGCCGTCCC	CCCCGCCGCC	TTCGCTTCGC	GGGTGCGGGC	CGGCGGGGTC	CTCTGACGCG	660
GCAGACAGCC	CTGCCTGTCT	CCTCCAGTGG	TTGTCTGACT	GCGGGCGGCC	CCCCTCCGCG	720
GCGGTGGGGG	TGCCGTCCCC	CCGGCCCCGTC	GTGCTGCCCT	CTCGGGGGGG	GTTTGCGCGA	780
GCGTCCGGCT	CGCCTGGGCC	CTTGCGGTGC	TCCTGGAGCG	CTCCGGGTTG	TCCCTCAGGT	840
GCCCCAGGCC	GAACGGTGGT	GTGTCTGTTT	CGCCCCCGGC	GCCCCCTCCT	CCGCTCGCCG	900
CCGCGGTGTC	CGCGCGTGGG	TCCTGAGGGA	GCTCGTCCGT	GTGGGGTTTC	AGGCGGTTTG	960
AGTGAGACGA	GACGAGACGC	GCCCCCTCCA	CGCGGGGAAG	GGCGCCCGCC	TGCTCTCGGT	1020
GAGCGCACGT	CCCGTGCTCC	CCTCTGGCGG	GTGCGCGCGG	GCCGTGTGAG	CGATCGCGGT	1080
GGGTTCTGGG	CGGTGTGACG	CGTGCGCCGG	CCGGCCCGCG	AGGGGCTGCC	GTTCTGCCTC	1140
CGACCGGTCT	TGTGTGGGTT	GACTTCGGAG	GCGCTCTGCC	TCGGAAGGAA	GGAGGTGGGT	1200
GGACGGGGGG	GCCTGGTGGG	GTTGCGCGCA	CGCGCGCACC	GGCCGGGGCC	CCGCCCTGAA	1260
CGCGAACGCT	CGAGGTGGCC	GCGCGCAGGT	GTTTCCTCGT	ACCGCAGGGC	CCCCTCCCTT	1320
CCCCAGGCGT	CCCTCGGCGC	CTCTGCGGGC	CCGAGGAGGA	GCGGCTGGCG	GGTGGGGGGA	1380
GTGTGACCCA	CCCTCGGTGA	GAAAAGCCTT	CTCTAGCGAT	CTGAGAGGCG	TGCCTTGGGG	1440
GTACCGGATC	CCCCGGGGCG	CCGCCTCTGT	CTCTGCCCTC	GTTATGGTAG	CGTGCCTGTA	1500
GCGACCCGCT	CGCAGAGGAC	CCTCCTCCGC	TTCCCCCTCG	ACGGGGTTTG	GGGGGAGAAG	1560
CGAGGGTTCC	GCCGGGCCAC	GCGGTGGTGG	CCGAGTGCGG	CTCGTCGCC	ACTGTGGCCC	1620
GCGCCTCCCC	CTTCCGAGTC	GGGGGAGGAT	CCCGCCGGGC	CGGGCCCGGC	GCTCCCACCC	1680
AGCGGGTTGG	GACGCGGCGG	CCGGCGGGCG	GTGGGTGTGC	GCGCCCGGCG	CTCTGTCCGG	1740



CGCGTGACCC	CCTCCGTCCG	CGAGTCGGCT	CTCCGCCCGC	TCCCGTGCCG	AGTCGTGACC	1800
GGTGCCGACG	ACCGCGTTTG	CGTGGCACGG	GGTGGGGCCC	GCCTGGCCCT	GGGAAAGCGT	1860
CCCACGGTGG	GGGCGCGCCG	GTCTCCCGGA	GCGGGACCGG	GTCGGAGGAT	GGACGAGAAT	1920
CACGAGCGAC	GGTGGTGGTG	GCGTGTCGGG	TTCGTGGCTG	CGGTGCGTCC	GGGGCCCCCG	1980
GTGGCGGGGG	CCCGGGGGCTC	GCGAGGCGGT	TCTCGGTGGG	GGCCGAGGGC	CGTCCGGCGT	2040
CCCAGGCGGG	GCGCCGCGGG	ACCGCCCTCG	TGTCTGTGGC	GGTGGGATCC	CGCGGCGCGT	2100
TTTTCTGGT	GGCCCCGGCCG	TGCTTGAGGT	TTCTCCCCGA	GCCGCCGCTT	CTGCGGGCTC	2160
CCGGGTGCCC	TTGCCCTCGC	GGTCCCCGGC	CCTCGCCCGT	CTGTGCCCTC	TTCCCCGCCC	2220
GCCGCCCGCC	GATCCTCTTC	TTCCCCCCGA	GCGGCTCACC	GGCTTCACGT	CCGTGCGTGG	2280
CCCCGCCTGG	GACCGAAACC	GGCACCGCCT	CGTGGGGCGC	CGCCGCCGGC	CACTGATCGG	2340
CCCGGCGTCC	GCGTCCCCCG	GCGCGCGCCT	TGGGGACCGG	GTCGGTGGCG	CGCCGCGTGG	2400
GGCCCCGGTGG	GCTTCCCCGA	GGGTTCGGGG	GGTGGCCCTG	CGGCGCGTGC	GGGGGAGGAG	2460
ACGGTTCCGG	GGGACCGGCC	GCGGCTGCGG	CGGCGGCGGT	GGTGGGGGGA	GCCGCGGGGA	2520
TCGCCGAGGG	CCGGTCGGCC	GCCCCGGGTG	CCCCGCGGTG	CCGCCGGCGG	CGGTGAGGCC	2580
CCGCGCGTGT	GTCCCCGGCTG	CGGTGCGGCC	CGCTCGAGGG	GTCCCCGTGG	CGTCCCCCTC	2640
CCCGCCGGCC	GCCTTTCTCG	CGCCTTCCCC	GTCGCCCCGG	CCTCGCCCGT	GGTCTCTCGT	2700
CTTCTCCCCG	CCCGCTCTTC	CGAACC GG GT	CGGCGCGTCC	CCCGGGTGCG	CCTCGCTTCC	2760
CGGGCCTGCC	GCGGCCCTTC	CCCGAGGCGT	CCGTCCCCGG	CGTCGGCGTC	GGGGAGAGCC	2820
CGTCCCTCCCC	GCGTGGCGTC	GCCCCGTTCG	GCGCGCGCGT	GCGCCCCGAG	GCGGCCCGGT	2880
GGTCCCTCCC	GGACAGGCGT	TCGTGCGACG	TGTGGCGTGG	GTCGACCTCC	GCCTTGCCGG	2940
TCGCTCGCCC	TCTCCCCGGG	TCGGGGGGTG	TGGCCCGGGC	CGGGGCCCTCG	GCCCCGGTCG	3000
CTGCCTCCCG	TCCCGGGCGG	GGGCGGGCGC	GCCGGCCGGC	CTCGGTGCGC	CTCCCTTGCG	3060
CGTCGTGTGG	CGTGTGCCAC	CCCTGCGCCG	GCGCCCCCGG	GCGGGGCTCG	GAGCCGGGCT	3120
TCGGCCGGGG	CCCGGGCCCT	CGACCGGACC	GGCTGCGCGG	GCGCTGCGGC	CGCACGGCGC	3180
GACTGTCCCC	GACTGTCCCC	CCGCGGTCCG	GCTCTGCTCC	GCCGCCCGGA	CGTCGGGGCC	3240
GCCCCGCGGG	GCGGGCGGAG	CGCCGTCCCC	GCCTCGCCGC	CGCCCGCGGG	CGCCGGCCGC	3300
GCGCGCGCGC	GCGTGGCCGC	CGGTCCCTCC	CGGCCGCGCG	GCGCGGGTCG	GGCCGTCCGC	3360
CTCCTCGCGG	GCGGGCGCGA	CGAAGAAGCG	TCGCGGGTCT	GTGGCGCGGG	GCCCCCGGTG	3420
GTCTGTTCGG	GTGGGGGGCG	GGTGGTTGGG	GCGTCCGGTT	CGCCGCGCCC	CGCCCCGGCC	3480
CCACCGGTCC	CGGCCGCGCG	CCCCGCGCCC	GCTCGCTCCC	TCCCGTCCCG	CCGTCCGCGG	3540
CCCGTCCGTC	CGTCCGTCCG	TCGTCCCTCT	CGCTTGCGGG	GCGCCGGGCC	CGTCCCTCGC	3600
AGGCCCCCCG	GCCGGCCGTC	CGGCCGCGTC	GGGGGCTCGC	CGCGCTCTAC	CTTACCTACC	3660
TGGTTGATCC	TGCCAGTAGC	ATATGCTTGT	CTCAAAGATT	AAGCCATGCA	TGTCTAAGTA	3720
CGCAGCGCCG	GTACAGTGAA	ACTGCGAATG	GCTCATTAAA	TCAGTTATGG	TTCTTTTGGT	3780
CGCTCGCTCC	TCTCCTACTT	GGATAACTGT	GGTAATTCTA	GAGCTAATAC	ATGCGGACGG	3840
GCGCTGACCC	CCTTCGCGGG	GGGGATGCGT	GCATTTATCA	GATCAAAACC	AACCCGGTCA	3900
GCCCCCTCTC	GGCCCCGGCC	GGGGGGCGGG	CGCCGGCGGC	TTTGGTGACT	CTAGATAACC	3960
TCGGGGCCGAT	CGCACGCCCC	CCGTGGCGGG	GACGACCCAT	TCGAACGTCT	GCCCTATCAA	4020
CTTTTCGATG	TAGTCCCGGT	GCCTACCATG	GTCAGCACGG	GTGACGGGGA	ATCAGGGTTC	4080
GATTCCGGAG	AGGAGGCCTG	AGAAACGGCT	ACCACATCCA	AGGAAGGCAG	CAGGCGCGCA	4140
AATTACCCAC	TCCCGACCCG	GGGAGGTAGT	GACGAAAAAT	AACAATACAG	GACTCTTTTC	4200
AGGCCCTGTA	ATTGGAATGA	GTCCACTTTA	AATCCTTTAA	CGAGGATCCA	TTGGAGGGCA	4260
AGTCTGGTGC	CAGCAGCCCG	GGTAATTCCA	GCTCCAATAG	CGTATATTAA	AGTTGCTGCA	4320
GTTAAAAAGC	TAGTAGTTGG	ATCTTGGGAG	CGGGCGGGCG	GTCCGCGCGC	AGGCGAGCCA	4380
CCGCCCGTCC	CCGCCCTTTG	CCTCTCGGCG	CCCCCTCGAT	GCTCTTAGCT	GAGTGTCCCG	4440
CGGGGCCCGA	AGCGTTTACT	TTGAAAAAAT	TAGAGTGTTT	AAAGCAGGCC	CGAGCCGCCCT	4500
GGATACCGCA	GCTAGGAATA	ATGGAATAGG	ACCGCGGTTT	TATTTTGTGG	GTTTTCGGAA	4560
CTGAGGCCAT	GATTAAGAGG	GACGGCCGGG	GGCATTCTGA	TTGCGCCGCT	AGAGGTGAAA	4620
TTCTTGGACC	GGCGCAAGAC	GGACCAAGAC	GAAAGCATTT	GCCAAGAATG	TTTTCATTAA	4680
TCAAGAACGA	AAGTCGGAGG	TTCGAAGACG	ATCAGATACC	GTCGTAGTTC	CGACCATAAA	4740
CGATGCCGAC	CGGCGATGCG	GCGGCGTTAT	TCCCATGACC	CGCCGGGCAG	CTTCCGGGAA	4800
ACCAAAGTCT	TTGGGTTCCG	GGGGGAGTAT	GGTTGCAAA	CTGAACTTA	AAGGAATTGA	4860
CGGAAGGGCA	CCACCAGGAG	TGGAGCCTGC	GGCTTAATTT	GACTCAACAC	GGGAAACCTC	4920
ACCCGGCCCC	GACACGGACA	GGATTGACAG	ATTGATAGCT	CTTTCTCGAT	TCCGTGGGTG	4980
GTGGTGCATG	GCCGTTCTTA	GTTGGTGGAG	CGATTTGTCT	GGTTAATTCC	GATAACGAAC	5040
GAGACTCTGG	CATGCTAACT	AGTTACGCGA	CCCCCGAGCG	GTCGGCGTCC	CCCAACTTCT	5100
TAGAGGGACA	AGTGGCGTTC	AGCCACCCGA	GATTGAGCAA	TAACAGGTCT	GTGATGCCCT	5160
TAGATGTCCG	GGGTGTCACG	GCGCTACAC	TGACTGGCTC	AGCGTGTGCC	TACCTTACGC	5220
CGGCAGGCGC	GGGTAACCCG	TTGAACCCCA	TTCGTGATGG	GGATCGGGGA	TTGCAATTAT	5280
TCCCCATGAA	CGAGGGAATT	CCCGAGTAAG	TGCGGGTCAT	AAGCTTGCGT	TGATTAAAGTC	5340
CCTGCCCTTT	GTACACACCG	CCCGTCGCTA	CTACCGATTG	GATGGTTTAG	TGAGGCCCTC	5400
GGATCGGGCC	CGCCGGGGTC	GGCCACGGCC	CCTGGCGGAG	CGCTGAGAAG	ACGGTCGAAC	5460
TTGACTATCT	AGAGGAAGTA	AAAGTCGTAA	CAAGTTTTCC	GTAGGTGAAC	CTGCGGAAGG	5520
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CTCCGCACAC	CCACCCCCCC	ACCGCGACGC	GGCGCGTGCG	CGGGCGGGGC	CCGCGTGCCC	5640
GTTCGTTTCG	TCGCTCGTTC	GTTCCGCCGC	CGGCCCCGCC	GCCGCGAGAG	CCGAGAACTC	5700
GGGAGGGAGA	CGGGGGGGAG	AGAGAGAGAG	AGAGAGAGAG	AGAGAGAGAG	AGAGAGAGAA	5760



AGAAGGGCGT	GTCGTTGGTG	TGCGCGTGTC	GTGGGGCCGG	CGGGCGGCGG	GGAGCGGTCC	5820
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GCGGCGGGTC	TGGGGGGGTC	TCGGTGCCCT	CCTCCCCGCC	GGGGCCCGTC	GTCCGGCCCC	5940
GCCGCGCCGG	CTCCCCGTCT	TCGGGGCCGG	CCGGATTCCC	GTCGCTCCG	CCGCGCCGCT	6000
CCGCGCCGCC	GGGCACGGCC	CCGCTCGCTC	TCCCCGGCT	TCCCGCTAGG	GCGTCTCGAG	6060
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GTACCTAGCG	CGTTCCGGCG	CGGAGGTTTA	AAGACCCCTT	GGGGGGATCG	CCCGTCCGCC	6180
CGTGGGTGCG	GGGCGGTGGT	GGGCCCCGCG	GGGAGTCCCG	TCGGGAGGGG	CCCGGCCCTT	6240
CCCGCGCCTC	CACCGCGGAC	TCCGCTCCCC	GGCCGGGGCC	GCGCCGCGCG	CGCCGCGCGG	6300
GCGGCCGTCG	GGTGGGGGCT	TTACCCGGCG	GCCGTGCGCG	GCCTGCCGCG	CGTGTGGCGT	6360
GCGCCCCGCG	CCGTGGGGGC	GGGAACCCCC	GGGCGCCTGT	GGGGTGGTGT	CCGCGCTCGC	6420
CCCCCGCTGG	GCGGCGCGCG	CCTCCCCGTG	GTGTGAAACC	TTCCGACCCC	TCTCCGGAGT	6480
CCGGTCCCGT	TTGCTGTCTC	GTCTGGCCGG	CCTGAGGCAA	CCCCCTCTCC	TCTTGGGCGG	6540
GGGGGGCGGG	GGGACGTGCC	GCGCCAGGAA	GGGCCTCCTC	CCGGTGCGTC	GTCGGGAGCG	6600
CCCTCGCCAA	ATCGACCTCG	TACGACTCTT	AGCGGTGGAT	CACTCGGCTC	GTGCGTCGAT	6660
GAAGAACGCA	GCTAGCTGCG	AGAATTAATG	TGAATTGCAG	GACACATTGA	TCATCGACAC	6720
TTCGAACGCA	CTTGCGGCCC	CGGGTTCCTC	CCGGGGCTAC	GCCTGTCTGA	GCGTGCCTTG	6780
CCGATCAATC	GCCCCGGGGG	TGCCTCCGGG	CTCCTCGGGG	TGCGCGGCTG	GGGGTTCCCT	6840
GCGAGGGCCC	GCCGCGGGCC	CTCCGTCCCC	CTAAGCGCAG	ACCCGGCGGC	GTCCGCCCTC	6900
CTCTTGCCCG	GCGCCCCGCC	CCTTCCCCCT	CCCCCGCGG	GCCCTGCGTG	GTACGCGCTC	6960
GGGTGGCGGG	GCGGAGAGGG	GGGCGCGCCC	GGCTGAGAGA	GACGCGGAGG	GCGGCGCCGC	7020
CGCCGGAAGA	CGGAGAGGGA	AAGAGAGAGC	CGGCTCGGGC	CGAGTTCCTG	TGGCCGCCGC	7080
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GGTTCGTCCG	CCCCGGCCGG	GTGGAAGGTC	CCGTGCCCTG	CGTCGTCTGC	GTCGCGCGTC	7200
GTCGGCGGTG	GGGGCGTGT	GCGTGCCTGT	TGGTGGTGGG	GGAGGAGGAA	CGCGGGTCCG	7260
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CGGGACGCCG	CGGTGTCGTC	CGCCGTGCGG	CGCCCGCCTC	CGGCTCGCGG	CCGCGCCGCG	7620
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CTCGGACCCG	TCCCCCCGAC	CTCCGCGGGG	GAGACGCGCC	GGGCGGTGCG	GCGCCCGTCC	7740
CGCCCCCGGG	CCGTGCCCTT	CCCTCCGGTC	GTCCCGCTCC	GGCGGGGCGG	GCGGGGGCGG	7800
CCGTGCGGCC	CGCGTCTCTT	CTCCCGTCCG	CTCTCCCCCT	CGCCGGGCCC	GCTCTCCGAC	7860
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GCGGCGGGTC	CGGCCGTGTC	GGCGGCCCGG	CGGATCTTTC	CCGCCCCCCG	TTCTTCCCGA	8460
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GTCGCGCCGT	CGGGCCCCGG	GGAGGTTCTC	TGGGGGCCAC	GCGCGCGTCC	CCCAAGAGG	9180
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TGAAACACGG	ACCAAGGAGT	CTAACACGTC	GCGGAGTCGG	GGGCTCGCAC	GAAAGCCGCC	9300
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TCCAGTCCGC	CGAGGGCGCA	CCACCGGCCC	GTCTCGCCCC	CCGCGCCGGG	GAGGTGGAGC	9420
ACGAGCGCAC	GTGTTAGGAC	CCGAAAGATG	GTGAACATAT	CCTGGGCAGG	GCGAAGCCAG	9480
AGGAAACTCT	GGTGGAGGTC	CGTAGCGGTC	CTGACGTGCA	AATCGGTCGT	CCGACCTGGG	9540
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GGATAGCTGG	CGCTCTCGCA	GACCCGACGC	ACCCCGCCCA	CGCAGTTTGA	TCCGGTAAAG	9660
CGAATGATTA	GAGGTCTTGG	GGCCGAAACG	ATCTCAACCT	ATTCTCAAAC	TTTAAATGGG	9720
TAAGAAGCCC	GGCTCGCTGG	CGTGGAGCCG	GGCGTGGAAT	GCGAGTGCCT	AGTGGGCCAC	9780

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TGGAAGTCGG	AATCCGCTAA	GGAGTGTGTA	ACAACCTACC	TGCCGAATCA	ACTAGCCCTG	9960
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CGCGCGCGGC	GGCGGGGGTG	TGGGGTCTTT	CCCCCGCCCC	CCCCCCCCACG	CCTCCTCCCC	10140
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CAGGTGCAGA	TCTTGGTGGT	AGTAGCAAAT	ATTCAAACGA	GAACCTTTGAA	GGCCGAAGTG	10320
GAGAAGGGTT	CCATGTGAAC	AGCAGTTGAA	CATGGGTTCAG	TCGGTCTCTGA	GAGATGGGCG	10380
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CCCCCGCCCC	ACCCGCGCGC	GCCGCTCGCT	CCCTCCCCAC	CCCGCGCCCT	CTCTCTCTCT	10980
CTCTCCCCCG	CTCCCCGTCC	TCCCCCTTCC	CCGGGGGAGC	GCCGCGTGGG	GGCGGCGCGG	11040
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AGGTCCCCGC	GAGGGGGGCC	CCGGGGACCC	GGGGGGCCCG	CGGCGGCGCG	GACTCTGGAC	11160
GCGAGCCGGG	CCCTTCCCGT	GGATCGCCCC	AGCTGCGGCG	GGCGTCGCGG	CCGCCCCCGG	11220
GGAGCCCGGC	GGCGGCGCGG	CGCGCCCCCC	ACCCCAACCC	CACGTCTCGG	TCGCGCGCGC	11280
GTCCGCTGGG	GGCGGGAGCG	GTCGGGCGGC	GGCGGTTCGG	GGGCGGCGGG	GCGGGGCGGT	11340
TCGTCCCCCC	GCCCTACCCC	CCCGGCCCCG	TCCGCCCCCC	GTTCCCCCCT	CCTCCTCGGC	11400
GCGCGGCGCG	GGCGGCGGCA	GGCGGCGGAG	GGGCCGCGGG	CCGGTCCCCC	CCGCCGGGTC	11460
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AGGCCCTGCC	CAGGACAGGC	AGGCAGGCAG	CGAGGCAGAA	AGACAACAGC	TGTATTATGT	36480
TCTTCTCAGG	GTAGGAAGCA	AAAATAACAG	AATACAGCAC	TTAATTAATT	TTTTTTTTTT	36540
CCTTCGGACG	GAGTTTCACT	CTTGGTGCCC	ACGCTGGAGT	GCAGTGGCAC	CATCTCGGCT	36600
CACCGCAACC	TCCACCTCCC	GCGTTCAAGC	GATTCTCCTG	CCTCAGCCTC	CTGAGTAGCT	36660
GGGATTACAG	GGAGGAGCCA	CCACACCCAG	CTGATTTTGT	ATTGTTAGTA	GAGACGGCAT	36720
TTCTCCATGT	GGGTCAAGCT	GGTCTCGAAC	TGGCCAGCCC	AGTGGATCTG	CCCGCCCGCG	36780
CCTCCCAAAG	TGCTGGGGTG	ACAGGCGTGA	GCCATCGTGA	CTGGCCGGCT	ACGTTTATTT	36840
ATTTATTTTT	TTAATTATTT	TACTTTTTTT	TAGTTTTCCA	TTTTAATCTA	TTTATTTATT	36900
TACATTTATT	TATTTATTTA	TTTATTTACT	TATTTATTTA	TTTTTCGAGAC	AGACTCTCGC	36960
TCTGCTGCCC	AGGCTGGAGT	GCAGCGGCGT	GATCTCGGCT	CACTGCAACG	TCCGCTCTCC	37020
GGGTTACAGC	CATTCTCCTG	CCTCAGCCTC	CCAAGTAGCT	GGGACTACAG	GGGCCCCCCA	37080
CCGTGCCCGG	CTAACTTTTT	GTATTTTGAG	TAGAGATGGG	GTTTCACTGT	GGTAGCCAGG	37140
ATGGTCTCGA	TCTCCTGACC	CCGTGATCCG	TCCACCTCGG	CCTCCCAAAG	TGCTGGGATG	37200
ACAGGCGTGA	GCCACCGGCC	CCGGCCTATT	TATCTATTTA	TTAACTTTGA	GTCCAGGTTA	37260
TGAAACCAGT	TAGTTTTTGT	AATTTTTTTT	TTTTTTTTTT	TTTTTTGAGA	CGAGGTTTCA	37320
CCGTGTTGCC	AAGGCTTGGA	CCGAGGGATC	CACCGGCCCT	CGGCCTCCCA	AAAGTGGGGG	37380
GATGACAGGC	GCGAGCCTAC	CGCGCCCGGA	CCCCCCTTTT	CCCCTTCCCC	CGCTTGCTCT	37440
CCCGACAGAC	AGTTTTCACG	CAGAGCGTTT	GGCTGGCGTG	CTTAAACTCA	TTCTAAATAG	37500
AAATTTGGGA	CGTCAGCTTC	TGGCCTCAGC	GACTCTGAGC	CGAGGAGTCC	CCTGGTCTGT	37560
CTATCACAGG	ACCGTACACG	TAAGGAGGAG	AAAAATCGTA	ACGTTCAAAG	TCAGTCAATT	37620
TGTGATACAG	AAATACACGG	ATTACCCCAA	AACACAGAAA	CCAGTCTTTT	AGAAATGGCC	37680
TTAGCCCTGG	TGTCCGTGCC	AGTGATTCTT	TTCGGTTTGG	ACCTTGACTG	AGAGGATTCC	37740
CAGTCGGTCT	CTCGTCTCTG	GACGGAAGTT	CCAGATGATC	CGATGGGTGG	GGGACTTAGG	37800
CTCGTCCCCC	CCAGGAGCCC	TGGTCGATTA	GTTGTGGGGA	TCGCCTTGGA	GGGCGCGGTG	37860
ACCCATGTG	CTGTGGGAGC	CTCCATCCTT	CCCCCACCC	CCTCCCCAGG	GGGATCCCAA	37920



TTCAATCCGG	GCTGACACGC	TCACTGGCAG	GCGTCGGGCA	TCACCTAGCG	GTCACGTGTTA	37980
CTCTGAAAAC	GGAGGCCTCA	CAGAGGAAGG	GAGCACCAGG	CCGCCTGCGC	ACAGCCTGGG	38040
GCAACTGTGT	CTTCTCCACC	GCCCCGCCCC	CCACCTCCAA	GTTCTCCCT	CCCTTGTTGC	38100
CTAGGAAATC	GCCACTTTGA	CGACCGGGTC	TGATTGACCT	TTGATCAGGC	AAAAACGAAC	38160
AAACAGATAA	ATAAAATAAA	TAACACAAAA	GTAACATACT	AAATAAAATA	AGTCAATACA	38220
ACCCATTACA	ATACAATAAG	ATACGATACG	ATAGGATGCG	ATAGGATACG	ATAGGATACA	38280
ATACAATAGG	ATACGATACA	ATACAATACA	ATACAATACA	ATACAATACA	ATACAATACA	38340
ATACAATACA	ATACAATACG	CCGGGCGCGG	TGGCTCATGC	CTGTCTATCC	GTCACCTTTGG	38400
GATGCCGAGG	TGGACGCATC	ACCTGAAGTC	GGGAGTTGGA	GACAAGCCCC	ACCAACATGG	38460
AGAAATCCCC	TCTCAATTGA	AAATACAAAA	CTAGCCGGGG	GCGGTGGCAC	ATGCCTATAA	38520
TCCCAGCTGC	TAGGAAGGCT	GAGGCAGGAG	AATCGCTTGA	ACCTGGGAAG	CGGAGGTTGC	38580
AGTGAGCCGA	GATTGCGCCA	TCGCACTCCA	GTCTGAGCAA	CAAGAGCGAA	ACTCCGTCTC	38640
AAAAATAAAT	ACATAAATAA	ATACATACAT	ACATACATAC	ATACATACAT	ACATACATAC	38700
ATAAATTAAA	ATAAATAAAT	AAAATAAAT	AAATAAATGG	GCCCTGCGCG	GTGGCTCAAG	38760
CCTGTCTATC	CCTCACTTTG	GGAGGCCAAG	GCCGGTGGAT	CAAGAGGCGG	TCAGACCAAC	38820
AGGGCCAGTA	TGGTGAAACC	CCGTCTCTAC	TCACAATACA	CAACATTAGC	CGGGCGCTGT	38880
GCTGTGCTGT	ACTGTCTGTA	ATCCCAGCTA	CTCGGGAGGC	CGAGCTGAGG	CAGGAGAATC	38940
GCTTGAACCT	GGGAGGCGGA	GGTTGCAGTG	AGCCGAGATC	GCGCCACTGC	AACCCAGCCT	39000
GGGCGACAGA	GCGAGACTCC	GTCTCCAAAA	AATGAAAATG	AAAATGAAAC	GCAACAAAAT	39060
AATTAAAAAG	TGAGTTTCTG	GGGAAAAAGA	AGAAAAGAAA	AAAGAAAAAA	ACAACAAAAC	39120
AGAACAACCC	CACCGTGACA	TACACGTACG	CTTCTCGCCT	TTTCGAGCCT	CAACACAGTT	39180
AGGAATTATG	CGTGATTCT	TTTTTTAACT	TCATTTTATG	TTATTATCAT	GATTGATGTT	39240
TCGAGACGGA	GTCTCGGAGG	CCCGCCCTCC	CTGGTTGCC	AGACAACCCC	GGGAGACAGA	39300
CCCTGGCTGG	GCCCGATTGT	TCTTCTCTCT	GGTCAGGGGT	TTCTTGTCT	TTCTTCGTGT	39360
CTTTAACCCG	CGTGGACTCT	TCCGCCTCGG	GTTTGACAGA	TGGCAGCTCC	ACTTTAGGCC	39420
TTGTTGTTGT	TGGGGACTTT	CCTGATTCTC	CCCAGATGTA	GTGAAAGCAG	GTAGATTGCC	39480
TTGCCTGGCC	TTGCCTGGCC	TTGCCTTTTC	TTTCTTTCTT	TCTTTCTTTA	TTACTTTCTC	39540
TTTTTCTTCT	TCTTCTTCTT	CTTTTCTTTG	AGACAGAGTT	TCACTCTTGT	TGCCCAGGCT	39600
AGAGGGCAAT	GGCGCATCT	CGGCTCACCG	CACCCCTCCG	CTCCCAGGTT	CAAGCGATTC	39660
TCCTGCCTCA	GCCTCTGAT	TAGCTGGGAT	TACAGGCATG	GGCCACCGTG	CTGGCTGATG	39720
TTTGTACTTT	TAGTAGAGAC	GGTGTTTTTT	CATGTTGGTC	AGGCTGGTCT	CCCACTCCCA	39780
ACCTCAGGTG	GTCCGCCTGC	CTTAGCCTCC	CAAAGTGCTG	GGATGACAGG	CGTGCAACCG	39840
CGCCCAGCCT	CTCTCTCTCT	CTCTCTCTCT	CTCGCTCGCT	TGCTTGCTTG	CTTTCGTGCT	39900
TTCTTGCTTT	CCCGTTTCTT	TGCTTTCTTT	CTTCTTTCTG	TTTCTTTTCT	GCTTGCTTTT	39960
TTGCTTGCTT	GCTTGCTTTT	GTGCTTTCTT	GCTTTCTGTT	TTTCTTTCTT	TCTTTCTTTT	40020
TTTCTTTCTT	TTGTTTCTTT	CTTGCTTGCT	TTCTTGCTTG	CTTGCTTGCT	TTCTTGCTTT	40080
CTTGCTTTCC	TGTTTTCTTT	CTTCTTTCTT	TTCTTTTCTT	TCTTTCTTGC	TTGCTTTCTT	40140
GCTTGCTTGG	TTTTCGTGCTT	TCTTGTTTTT	TCGATTTCTT	TCTTTCTTTT	GTTTCTTTCC	40200
TGCTTGCTTT	CTTGCTTGCT	TGCTTTCTGT	CTTCTTGCTT	TCCTGTTTTT	TTTCTTGCTT	40260
TCTTTCTTTT	GTTTCTTTCT	TGCTTGCTTT	CTTGCTTGCT	TGCTTTCTGT	CTGTCTTGTT	40320
TCTCGATTTT	TTTCTTTCTT	TTGTTTCTTT	CCTGCTTGCT	TTCTTGCTTG	ATTGCTTTCT	40380
TGCTTTCTTG	CTTTCTTGTT	TTCTTTCTTT	CTTTTGTTTT	TTTCTTTCTT	GCTTCTTGTT	40440
TTTCTTGCTT	CTTGCTTGCT	TTGCTTTCTG	GCTTTCTTGT	TTTCTTGCTT	TCTTTCTTTT	40500
GTTTCTTTCT	TGCTTGCTTT	CTTGCTTCTT	TGTTTTCTTG	CTTTCTTGCT	TGCTTGCTTT	40560
CGTGCTTTCT	TTCTTGCTTT	CTTTTCTTTT	TTTCTTTTCT	TTTTCTTTCT	TTCTTGCTTT	40620
CTTTTCTTTT	ATCATCATCT	TTCTTTCTTT	CCTTTCTTTT	TTTCTTTCTT	TCTATCTTTT	40680
TTTCTTTCTT	TCTTTCTTTT	TTTCTTTCTT	TCTTTCTGTT	TCGTCCTTTT	GAGACAGAGT	40740
TTTCACTTTG	TTTCCACGGC	TAGAGTGCAA	TGGCTCGATC	TTGGCTCACC	GCACCTTCCG	40800
CCTCCCGGGT	TCGAGCGCTT	CTCCTGCCTC	CAGCCTCCCG	ATTAGCGGGG	ATTGACAGGG	40860
AGGCACCCCC	ACGCCTGGCT	TGGCTGATGT	TTGTGTTTTT	AGTAGGCACG	CCGTGTCTCT	40920
CCATGTTGCT	CAGGCTGGTC	TCCAACCTCC	GACCTCCTGT	GATGCGCCCA	CCTCGGCCTC	40980
TCGAAGTGCT	GGGATGACGG	GCGTGACGAC	CGTGCCCGGG	CTGTTGACTC	ATTTCTGCTT	41040
TTTATTTCTT	TCGTTTCCAC	GCGTTTACTT	ATATGTATTA	ATGTAAACGT	TTCTGTACGC	41100
TTATATGCAA	ACAACGACAA	CGTGTATCTC	TGCATTGAAT	ACTCTTGCGT	ATGGTAAATA	41160
CGTATCGGTT	GTATGGAAAT	AGACTTCTGT	ATGATAGATG	TAGGTGTCTG	TGTTATACAA	41220
ATAAATACAC	ATCGCTCTAT	AAAGAAGGGA	TCGTCGATAA	AGACGTTTAT	TTTACGTATG	41280
AAAAGCGTCG	TATTTATGTG	TGTAATGAA	CCGAGCGTAC	GTAGTTATCT	CTGTTTTCTT	41340
CTTCTCTCTC	CTTCGTGTTT	TTCTTCTCTT	CTTCTCTCTT	TTCTCTCTCT	TTTACGTTT	41400
TTCTTCTCTT	CTTCTTTTCC	TTCTTTCTCT	CTTCTGTGCT	TTTTTTCTCT	CGTGCTTTAT	41460
TTCTCTTTCT	TTCCCTGTGT	TTCTTTCTTT	TTTCTTTCTT	CTCTGTTTCT	TTTTCCCTTC	41520
TTTCTTTCTG	TTCTTTCTCT	ATTCTTTCTC	TCTTTTCTGT	TGTTTCTTTT	CTTCCCCTCT	41580
GTCTTTTAAA	AAATTGGAGT	GTTTCAGAAG	TTTACTTTGT	GTATCTACGT	GTATCTAAAT	41640
GTCTCTCTTT	TCTCCATTTT	CTTCTCTCTT	CCCTCCCTCC	CTCCCTGCTC	CCTTCCCTCC	41700
CTCCTTCCCT	TTCCGCATCT	GTCTCTTTTC	CCCACTCCCC	TCCCCCGGTC	TGTCTCTGCG	41760
TGGATTCCGG	AAGAGCCTAC	CGATTCTGCC	TCTCCGTGTG	TCTGCAGCGA	CCCCGCGACC	41820
GAGTCCTTGT	GTGTTCTTTT	TCCCTCCCTC	CCTCCCTCCC	TCCCTCCCTC	CCTCCCTGCT	41880
TCCGAGAGGC	ATCTCCAGAG	ACCGCGCCGT	GGGTTGTCTT	CTGACTCTGT	CGCGGTCGAG	41940

GCAGAGACGC	GTTTTGGGCA	CCGTTTGTGT	GGGGTTGGGG	CAGAGGGGCT	GCGTTTTTCGG	42000
CCTCGGGAAG	AGCTTCTCGA	CTCACGGTTT	CGCTTTCGCG	GTCCACGGGC	CGCCCTGCCA	42060
GCCGGATCTG	TCTCGCTGAC	GTCCGCGGCG	GTTGTCGGGC	TCCATCTGGC	GGCCGCTTTG	42120
AGATCGTGCT	CTCGGCTTCC	GGAGCTGCGG	TGGCAGCTGC	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	AGGCAGAGCT	CCGAAAGCC	CGCGTCTGTC	AGCCCGGCTG	GCCCGGTGGC	42240
GCCAGAGCTG	TGGCCGGTCG	CTTGTGAGTC	ACAGCTCTGG	CGTGCAGGTT	TATGTGGGGG	42300
AGAGGCTGTC	GCTGCGCTTC	TGGGCCCGCG	GCGGGCGTGG	GGCTGCCCGG	GCCGGTCCGAC	42360
CAGCGCGCCG	TAGCTCCCGA	GGCCCGAGCC	GCGACCCGGC	GGACCCGCCG	CGCGTGCGCG	42420
AGGCTGGGGA	CGCCCTTCCC	GGCCCGGTCT	CGGTCCGCTC	ATCCTGGCCG	TCTGAGGCGG	42480
CGGCCGAATT	CGTTTCCGAG	ATCCCCGTGG	GGAGCCGGGG	ACCGTCCCCG	CCCCGTCCCC	42540
CGGGTGCCCG	GGAGCGGTCC	CCGGGCCGGG	CCGCGTCCCC	TCTGCCGCGA	TCCTTTCTGG	42600
CGAGTCCCCG	TGGCCAGTCG	GAGAGCGCTC	CCTGAGCCGG	TGCGGCCCGA	GAGGTCCGCG	42660
TGGCCGGCCT	TCGGTCCCTC	GTGTGTCCCG	GTCGTAGGAG	GGGCCGGCCG	AAAATGCTTC	42720
CGGCTCCCCG	TCTGGAGACA	CGGGCCGGCC	CCTGCGTGTG	GCCAGGGCGG	CCGGGAGGGC	42780
TCCCCGGCCC	GGCGCTGTCC	CCGCGTGTCT	CCTTGGGTTG	ACCAGAGGGA	CCCCGGGCGC	42840
TCCGTGTGTG	GCTGCGATGG	TGGCGTTTTT	GGGGACAGGT	GTCCGTGTCC	GTGTCCGCGC	42900
TCGCCTGGGC	CGGCGGCGTG	GTCGGTGACG	CGACCTCCCC	GCCCCGGGGG	AGGTATATCT	42960
TTCGCTCCGA	GTCGGCAATT	TTGGGCCGCC	GGGTTATAT			42999

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 175 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCCGCGC	GCCCCCGTGT	TCGCCGTTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCAGT	GCCGTTGTGG	AGTGCCTCGC	TCTCCTCCTC	CTCCCCGGCA	120
CGGTTCCAC	GTTGGGGGAC	CACCGGTGAC	CTCGCCCTCT	TCGGGCCTGG	ATCCG	175

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 755 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGGAAC	GGCGGGGTCTG	60
GTCGTGCCCG	GCGCCGGACG	TGTGTCGGGG	CCCACTTCCC	GCTCGAGGGT	GGCGGTGGCG	120
GCGGCGTTGG	TAGTCTCCCG	TGTTGCGTCT	TCCCGGGCTC	TTGGGGGGGG	TGCCGTCGTT	180
TTCGGGGCGC	GCGTTGCTTG	GCTTACGCAG	GCTTGGTTTT	GGACTGCCTC	AGGAGTCGTG	240
GGCGGTGTGA	TTCCCGCCCG	TTTGCCTCG	CGTCTGCCTG	CTTTGCCTCG	GTTTGCTTG	300
GTTCTGTGCT	CGGGAGCGGT	GGTTTTTTTT	TTTTTCGGGT	CCCGGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCGTCGCC	CCCTGCCGCC	GGTGGGTTTT	CGTTTCGGGC	TGTGTTCTGTT	420
TCCCTTCCC	CGTTTCGCCG	TCGGTCTCTC	CCGGTCGGTC	GGCCCTCTCC	CCGGTCGGTC	480
GCCCGGCCGT	GCTGCCGGAC	CCCCCTTCT	GGGGGGGATG	CCCGGGCACG	CACGCGTCCG	540
GGCGGCCACT	GTGGTCCGGG	AGCTGCTCGG	CAGGCGGGTG	AGCCAGTTGG	AGGGGCGTCA	600
TGCCCCCGCG	GGCTCCCGTG	GCCGACGCGG	CGTGTTCTTT	GGGGGGGCCT	GTGCGTGCGG	660

GAAGGCTGCG CACGTTGTCG GTCCTTGCGA GGGAAAGAGG CTTTTTTTTT TTAGGGGGTC 720  
GTCCTTCGTC GTCCCGTCGG CGGTGGATCC GGCCT 755

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAGGTG	CGTCTGCGGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCCTCCG	GGAAGGCGTT	60
TAGCGGGTAC	CGTCGCCCGG	CCGAGGTGGG	CGCACGTCGG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGGCGGG	GGCTCCGGTC	GATGTCTTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAGCC	TCCGCCTGTG	GGCTTCGTCT	GCCGTCTCCC	CCCCCCTCAC	GTCCCTCGCG	240
AGCGAGCCCC	TCCGTTTCGAC	CTTCCTTCCG	CCTTCCCCCC	ATCTTTCCGC	GCTCCGTTGG	300
CCCCGGGGTT	TTCACGGCGC	CCCCCACGCT	CCTCCGCCCT	TCCGCCCGTG	GTTTGGACGC	360
CTGGTTCCGG	TCTCCCCGCC	AAACCCCGGT	TGGGTTGGTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGGTCTCCC	AACCCCGGCG	CGGAAGGGTT	CGGGGGTTCC	GGG		463

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCCT	TTCCGGCTCC	GGCCGGGGGG	60
GGCGGCCCCG	GGCGGTTTGG	TGAGTTAGAT	AACCTCGGGC	CGATCGCACG	CCCCCGTGG	120
CGGCGACGAC	CCATTGCAAC	GTCTGCCCTA	TCAACTTTCG	ATGGTAGTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTCGATTCC	GGAGAGGGAG	CCTGAGAAAC	240
GGCTACCACA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAT	ACAGGACTCT	TTCGAGGCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAAGCAG					378

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTCACCGC	CCGTCCCCGC	CCCTTGCCCTC	TCGGCGCCCC	CTCGATGCTC	180
TTAGCTGAGT	TGTCCCGCGG	GGCCCCAAGC	GTTTACTTTG	AAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCCC	GAGCCGCCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTTTGT	TTGGTTTTCG	GAAC TGAGCC	CATGATTAAG	GGAAACGGCC	GGGGGCATTC	360
CCTTATTGCG	CCCCCCTA					378

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 719 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTCC	CGCTCCCCGT	TCCTCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCTTCTTT	60
TCCCCTCTCC	GGAGGGGGGG	GAGGTGGGGG	CGCGTGGGCG	GGGTGCGGGG	TGGGGTCGGC	120
GGGGGACCGC	CCCCGGCCGG	CAAAAGGCCG	CCGCCGGGCG	CACTTCAACC	G TAGCGGTGC	180
GCCGCGACCG	GCTACGAGAC	GGCTGGGAAG	GCCCCACGGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGCGCC	GAACCACCTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCGGGGCC	GAGGGGAAGC	CCGATACCCG	TCGCCGCGCT	TTTCCCCTCC	360
CCCCGTCCGC	CTCCCGGGCG	GGCGTGGGGG	TGGGGGCCCG	GCCGCCCCCTC	CCACGCCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGGC	480
GGACTGTCCT	CAGTGCGCCC	CGGGCGTCGT	CGCGCCGTCG	GGCCCGGGGG	GTTCTCTCGG	540
TCACGCCCGA	CCCGACGAAG	CCGAGCGCAC	GGGTTCGGCG	GCGATGTCGG	CTACCCACCC	600
GACCCGTCTT	GAAACACGGA	CCAAGGAGTC	TAACGCGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCCG	TGGCGCAATG	AAGGTGAAGG	GCCCCGTCCG	GGGGCCCCGAG	GTGGGATCC	719

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 685 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT	CCAGTCCGCC	GAGGGCGCAC	CACCGGCCCG	TCTCGCCCGC	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAACTATGC	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	G TAGCGGTCC	TGACGTGCAA	ATCGGTGCTC	180
CGACCTGGGT	ATAGGGGCGA	AAGACTAATC	GAACCATCTA	G TAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTTATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCCGGA	AACGATCTCA	AACTATTTCT	CAAACCTTAA	360
ATGGGTAAAG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGCG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTTT	GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTTAAGGCGC	480
CCGATGCCGA	CGCTCATCAG	ACCCAGAAAG	AGGTGTTGGT	TGATATAGAC	AGCAGGACCG	540
TGGCCATGGA	AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTCGC	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	GCCGC				685

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG

35

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC

33

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCCT AACCCCTAACC CTAACCCTAA  
CCCTAACCCT AACCCGGGAT

60

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21